

AMENDMENTS TO THE DRAWINGS:

The attached sheet of drawings includes changes to Fig. 4. This sheet, which includes Fig. 4, replaces the original sheet including Fig. 4. In Fig. 4, the sequence of K11 phage, residues 690-761, (line 15 of Fig. 4) was slightly shifted in original Fig. 4. Accordingly, the correct sequence and alignment of this sequence are shown in the corrected Fig. 4.

Attachments: Replacement Sheet
Annotated Sheet Showing Changes



Fig. 4

T7 436: GNDMTKGLTLAKGPI - GREYYWLKIHGANCAGVDKVFPERI - KFIENHENI - MACAKSPLENTWAEQDSPP
T3 437:E.F.....-A..KHVDD..-L...D.IN.....
K11 459:S.....LD.F.....EG..-L.S.AD..N...TQ.....
SP6 427: S..LG.A..RFTTE.R.VN.V.ALK.FC.N..LW.W..KT.DV.VSNVLD.EFQDMCRDI.AD..TF.Q..KA.A.Y
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T7 513: AFCFEYA---GVOHHG-L-SYNCSLPLAFDSCSGTGHPSAMLRDEYVGGRAVNLPLSETVQDIYGIYAKKVNILQ
T3 514:T.....
K11 536:K.....-N.....ST.....D...K.D..V.HQ
SP6 507: W.....QYLDLWDE.RADEFRTH..VHQ.....AK..K..DAP.....A..O..-V-I
* * * * *
T7 588: NGTDNEVTVTDENTGEISEKVKLGTKALAGQWLAYGVTRSVTKRSVNTLAYGSKFGRQOVLEDTIQ-PAIDSGK
T3 589:P..MI...KD.....L...ST..Q.....D.....
K11 611: ..SQT.V.EQIA.KE..FH..T..ESV..A..O..K.....SLV.....-N.E
SP6 581: ALYMDADDA.TFTS.SVTLISGT-ELR.M.SA.DSI.I...L.KP....P...TRLTC.ES.IDXIVDLEEKAAQ.
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T7 667: FT-OPNOAAGYMAKLIWESVSVTVAAVEAMNWLKSAKLLAAEVKKKTGEILR---KRC-AHVHWTPDGFVPWQE
T3 668:DA.T.....K.....H.....I.....
K11 690: ..-H.....DA.T.....K.V.....I.....
SP6 660: EGRTA.KVHPFEDDRQDYLTPGAAYNYMT..LI.PSISEVVK.PI.AM.MIRQLA.FAA..NEGLMYTL.T..ILE.K
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T7 742: PIOTRLNLMFLGQFRLOPTINTNKDSEIDAHKQESGIAPNFVHSQDGHRLKTVVWAHEKYGIESFALIHDSFGTIP
T3 743: L.K.DMI.....L..G.....M..Y.....
K11 765: QN.A..K.V..ANYKM.Y..G.....M..H.N.V..D.....S..
SP6 740: TEML.VRTCLM.DIRMSLOVE---IV.EAAMMGAA.....GH.A..IL..CELVD..-VT.I.V.....HA
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T7 822: ANLEKAVRETWVDTYESCDVLADFYDQFADQLHESQDKMPALPAKGNLNLRLDLESDFAF
T3 823: GK.....I..NN.....T.....P..K...O..K.....
K11 845: G.....K..DN.I.....V...D.....
SP6 816: IT.RV.LKGO..AM.IDGNA.QKL-LE-EHEVR-WMV.TGIEV.EQ.EFD.NE.MD.EIV..
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T7 436: GNDMTKGLITLAKGPI--GKEGYWMLKIHGANCAGVDRKPPFPERI--KFTIENHENI--MACAKSPLENTWAEQDSFP
T3 437:E..F.....A..KHVDD..L.....D..IN.....
K11 459:S.....LD..F.....EG..L..S..AD..N.....TO.....
SP6 427: S..LG.A..RTE.R.VN.V.ALK.PC.N..LW.W..KT.DV.VSNULD.EFODMCRDI..AD..TF..Q..KA..A..Y
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T7 513: AFCEYA---GVQHHG-L-SYNCSLPLAFDSCSGIQHFSAMLRDEVGGRVNLPLSETVQDIYGIYAKVNEILOA
T3 514:T.....
K11 536:K.....N.....SI.....D.....K..D.....V..HQ
SP6 507: W.....OYLDLVD.E..RADEFRTH..VHQ.....Y.....AK.....K..DAP.....A..Q..--V-I
* * * * *
T7 588: NGTDNEVVVTVDENTGEISEKVKLGTKALAGOMLAYGVTSVTKSVMTLAYGSKFGRQOVLEDTIQ--PAIDSGK
T3 589:P..MI..KD.....L.....ST..Q.....D.....
K11 611: ..SQT.V.EQIA..KE..PH..T..ESV..A..Q.....K.....SLV.....N.E
SP6 581: ALYMDADDA.TFTS.SVTLSTG--ELR..M.SA.DSI..I..L..KP....P...TRLTC.ES.IDIYVDLEKEHAQ..
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T7 667: FT--OPNOAGYMAKLIVESVTVVAAVEAMNWLKSAKLIAAEVKDKKTGETLR---KRC-AVHWVTFDGPVWMBE
T3 668:DA.....K.....K.....H.....T.....
K11 690:DA..T.....K.....K.....I.....
SP6 660: EGRTA.KVHEFFEDDROLYLTFGAANYMT.L.I.PSISEVVK.P.I..AM.MIROIA.FAA..NEGMLMYTL.T..ILE.K
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K11 690:H.....DA..I.....K.V.....I.....* * * * *
T7 742: PIQTRILNMLFGFRLQPTINTNKDSEIDAHKQESGLAPNFVHSQDGSRLKRTVVWAHEKYGIESFALIHDSFGTIP
T3 743: ..L..K..DMI.....L.....G.....M..Y.....
K11 765: QN.A..K.V...ANVM.Y..G.....M..H.N.V..D.....S..
SP6 740: TEMPL.VRTCLM..DIKMSLOVE...--IV.EAAMMGAA.....CH.A..IL..CELVD..VT..I..V.....HA
* * * * *
T7 822: ANLFKAVRTHWDTYESCDVLADFYDQFADQLHESQDKMPALPAKGNINLRDILESDFAPA
T3 823: GK.....I...NN.....S.....T.....P..K.....Q..K..
K11 845: G.....K...DN..I.....V..D.....
SP6 816: LT.RV.LKGQ..AM.IDGNA.OKL-LE-EHEVR-WNV.TGIEV.EQ.EFD.NE.MD.EVY..
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